

SEQUENCE LISTING

<110> MIYATA, Toshio
KUROKAWA, Kiyoshi

<120> Megsin Protein

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<150> JP09-275302

<151> 1997-09-22

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<170> PatentIn Ver. 2.0

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<222> (1)..(1140)

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aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct	96
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser	
20 25 30	

ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat	144
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp	
35 40 45	

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca	192
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser	
50 55 60	

gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg	240
Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu	
65 70 75 80	

aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc	288
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu	
85 90 95	

agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag	336
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys	
100 105 110	

gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga	384
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg	
115 120 125	

gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys 130 135 140	432
tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu 145 150 155 160	480
ggg ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr 165 170 175	528
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aag att ctt gag ctg aga tac aat ggt ggc ata aac atg tac gtt ctg Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu 225 230 235 240	720
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aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val 260 265 270	816
gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys 275 280 285	864
caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys 290 295 300	912
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atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala 325 330 335	1008
act gct gcc aca gga agt aat att gta gaa aag caa ctg cct cag tcc Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser 340 345 350	1056
acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp 355 360 365	1104

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1143

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 35 40 45
 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
 50 55 60
 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
 65 70 75 80
 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
 85 90 95
 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
 100 105 110
 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
 115 120 125
 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
 130 135 140
 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
 145 150 155 160
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 165 170 175
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
 180 185 190
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
 195 200 205
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
 210 215 220
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
 225 230 235 240
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
 245 250 255

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Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
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Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
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Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
    290                      295                      300
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
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Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
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Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
    340                      345                      350
Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
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<222> (8)..(1147)

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tta ttc aga gag atg gat agt agt caa gga aac gga aat gta ttc ttc 97
Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe
  15                      20                      25                      30

tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct 145
Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala
        35                      40                      45

cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc 193
Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser
        50                      55                      60

cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat 241
Pro Ser Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr
        65                      70                      75

caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn 289
Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa
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aaa ctc agc att gcc aat gga gtt ttt gca gag aaa gta ttt gat ttt 337

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His	Lys	Ser	Tyr	Met 115	Glu	Cys	Ala	Glu	Asn 120	Leu	Tyr	Asn	Ala	Lys 125	Val	
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Glu	Arg	Val	Asp 130	Phe	Thr	Asn	Asp	Ile 135	Gln	Glu	Thr	Arg	Phe 140	Lys	Ile	
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Asn	Lys	Trp 145	Ile	Glu	Asn	Glu	Thr 150	His	Gly	Lys	Ile	Lys 155	Lys	Val	Leu	
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Ser	Lys	Leu 320	Met	His	Lys	Ser 325	Leu	Ile	Glu	Val	Ser 330	Glu	Glu	Gly	Thr	
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 35 40 45
 Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser
 50 55 60
 Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu
 65 70 75 80
 Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu
 85 90 95
 Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys
 100 105 110
 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg
 115 120 125
 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys
 130 135 140
 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp
 145 150 155 160
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 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser
 180 185 190
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 195 200 205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met
 210 215 220
 Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met
 225 230 235 240
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 245 250 255
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 260 265 270
 Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg
 275 280 285
 Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg
 290 295 300
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<220>
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 ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg 96
 Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
 20 25 30
 ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt 144
 Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
 35 40 45
 aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt 192
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
 50 55 60

cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag	240
Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys	
65 70 75 80	
gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat	288
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr	
85 90 95	
gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct	336
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala	
100 105 110	
aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt	384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe	
115 120 125	
aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag	432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys	
130 135 140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg	480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val	
145 150 155 160	
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act	528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr	
165 170 175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta	576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val	
180 185 190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag	624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln	
195 200 205	
cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc	672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser	
210 215 220	
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Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys	
225 230 235 240	
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Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys	
245 250 255	
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Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn	
260 265 270	
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Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe	
275 280 285	
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc	912
Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu	
290 295 300	


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305 310 315 320

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Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln
325 330 335

ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc 1056
Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val
340 345 350

atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct 1104
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<213> Mus musculus

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Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
50 55 60

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys
65 70 75 80

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr
85 90 95

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala
100 105 110

Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe
115 120 125

Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys
130 135 140

Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val
145 150 155 160

Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr
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Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val

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<220>
<223> Description of Artificial Sequence:synthesis

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<210> 11
<211> 18
<212> DNA
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<220>
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<220>
<223> Description of Artificial Sequence:synthesis

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<220>
<223> Description of Artificial Sequence:synthesis

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<220>
<223> Description of Artificial Sequence:synthesis

<400> 25
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<210> 26
<211> 26
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<220>
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<400> 26
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<210> 27
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<220>
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<400> 27
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<210> 28
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<400> 28
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34

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<400> 29
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30

<210> 30
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27

<210> 31
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36

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<220>
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19

<210> 33
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<220>
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<400> 33
gaaacaaatc aaagcaaac 19

<210> 34
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<210> 35
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<400> 35
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<210> 36
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<220>
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<400> 36
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<210> 37
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<220>
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<400> 37
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<210> 38
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<400> 38
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<210> 39
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<213> Artificial Sequence

<220>
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<400> 39
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<210> 40
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<400> 40
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<210> 41
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<400> 41
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<400> 42
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<210> 43
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<220>
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44

<210> 44
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<212> DNA
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<220>
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<400> 44
tatactgagg cagtgttaac aagcaac

27